

FIGURE 2

199A
Probe-Array Analysis
Applications Executables
(with related data structures)

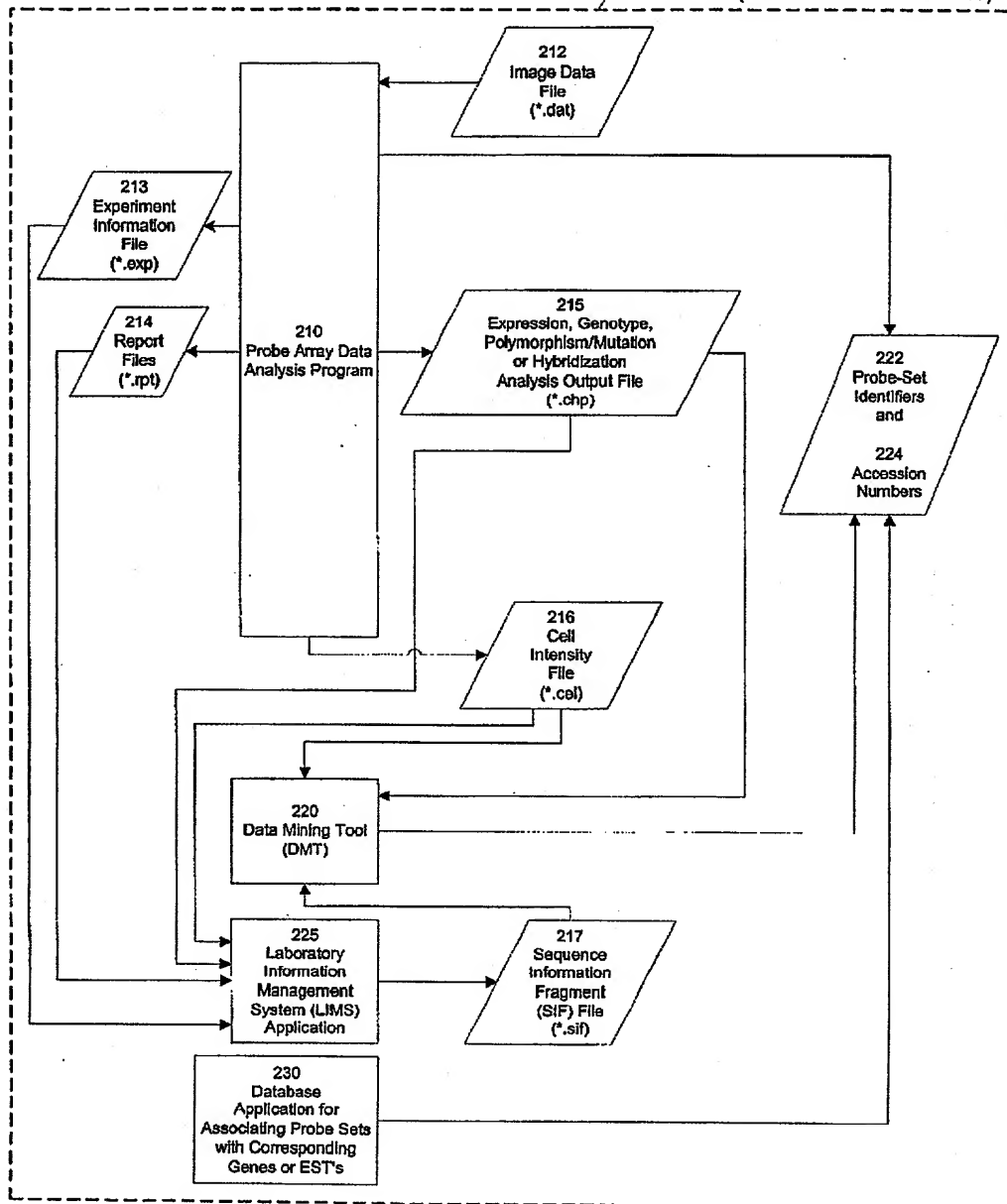


FIGURE 3
(PRIOR ART)

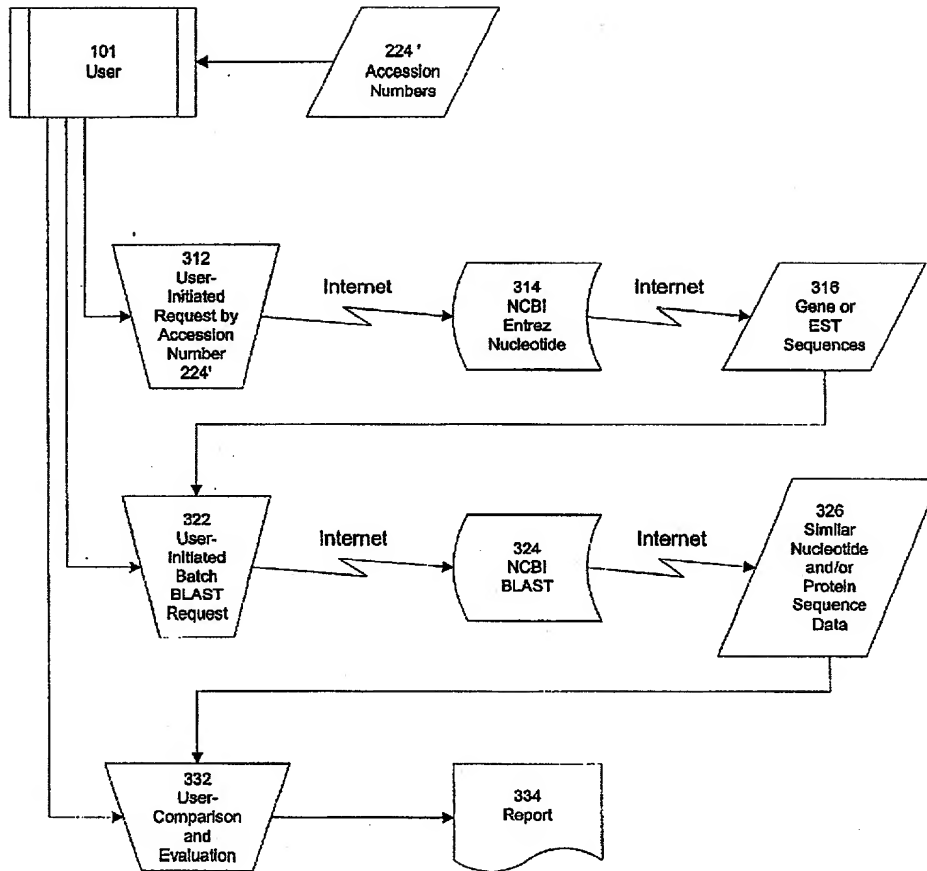


FIGURE 4

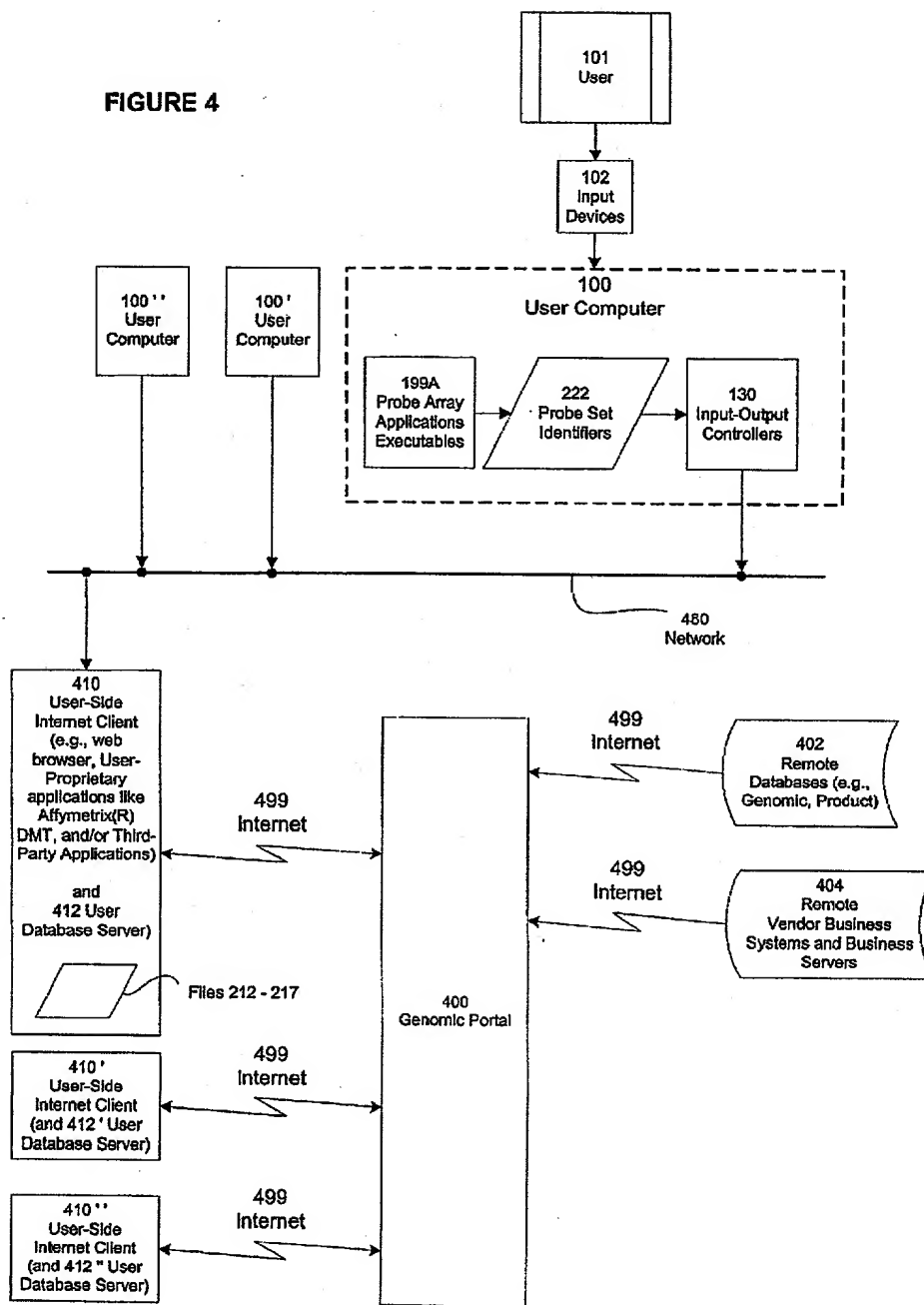


FIGURE 5

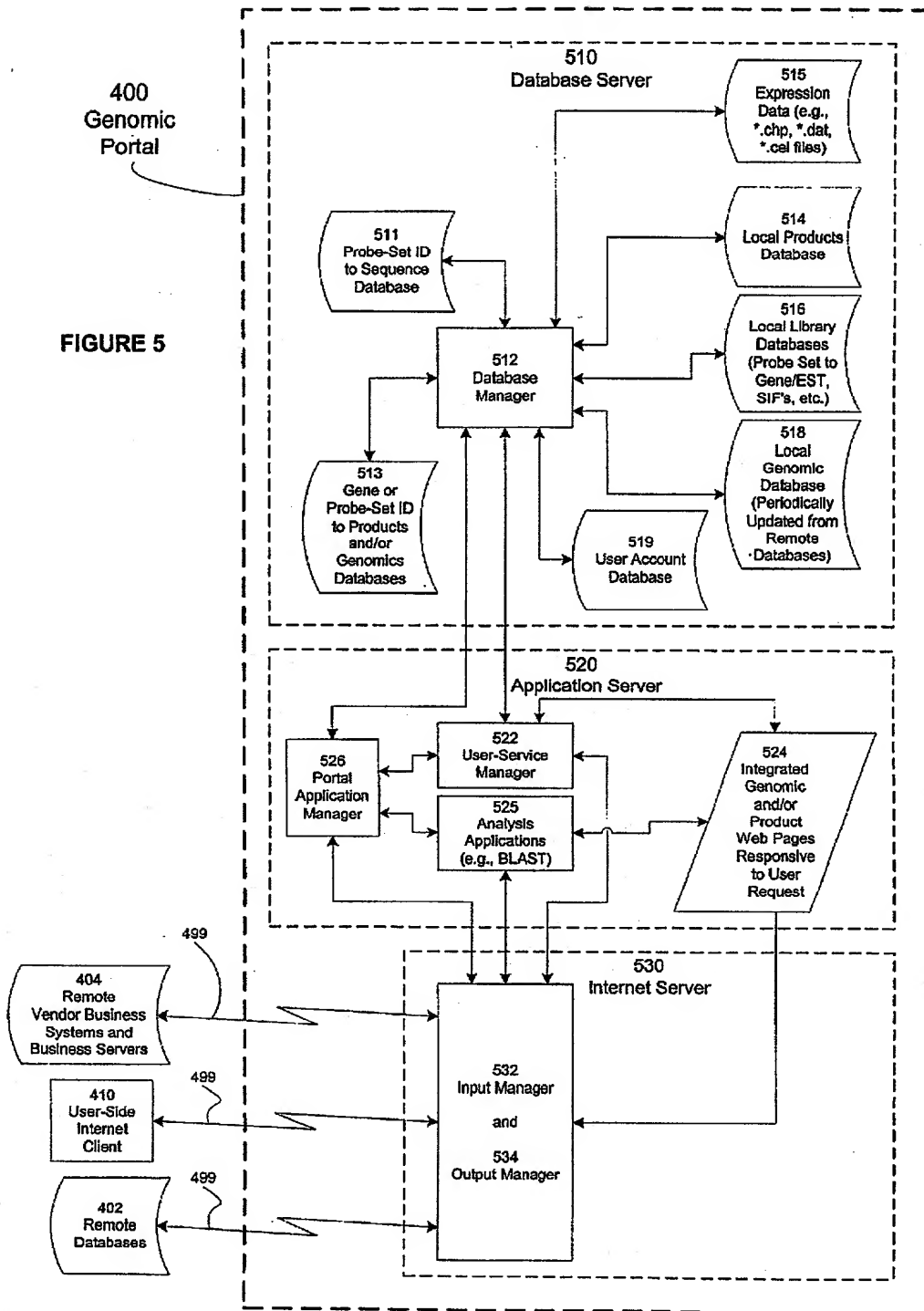


FIGURE 6

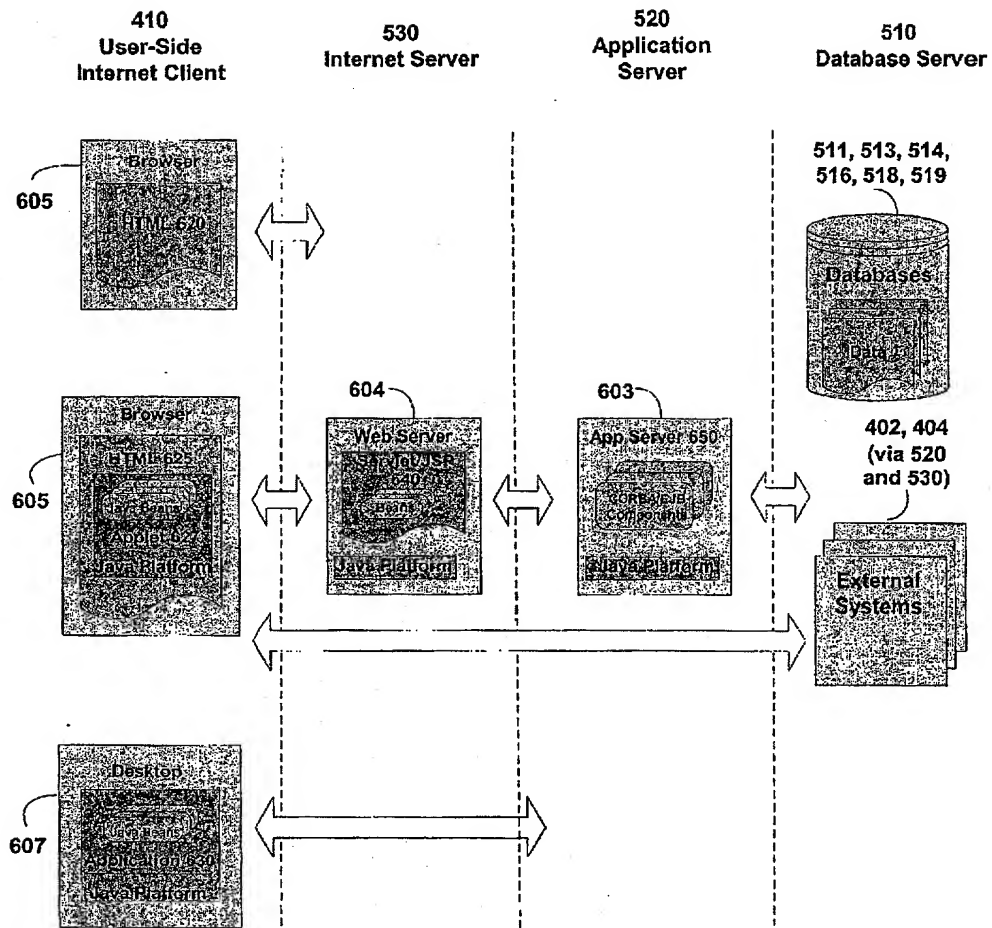


FIGURE 7

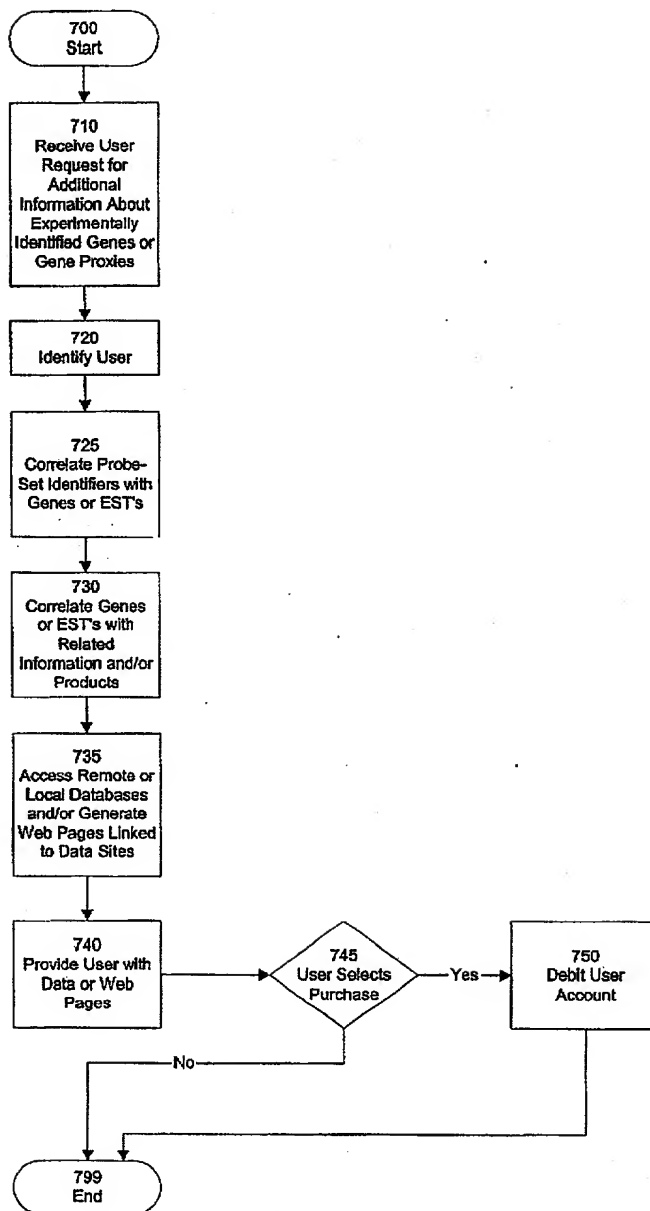


FIGURE 8

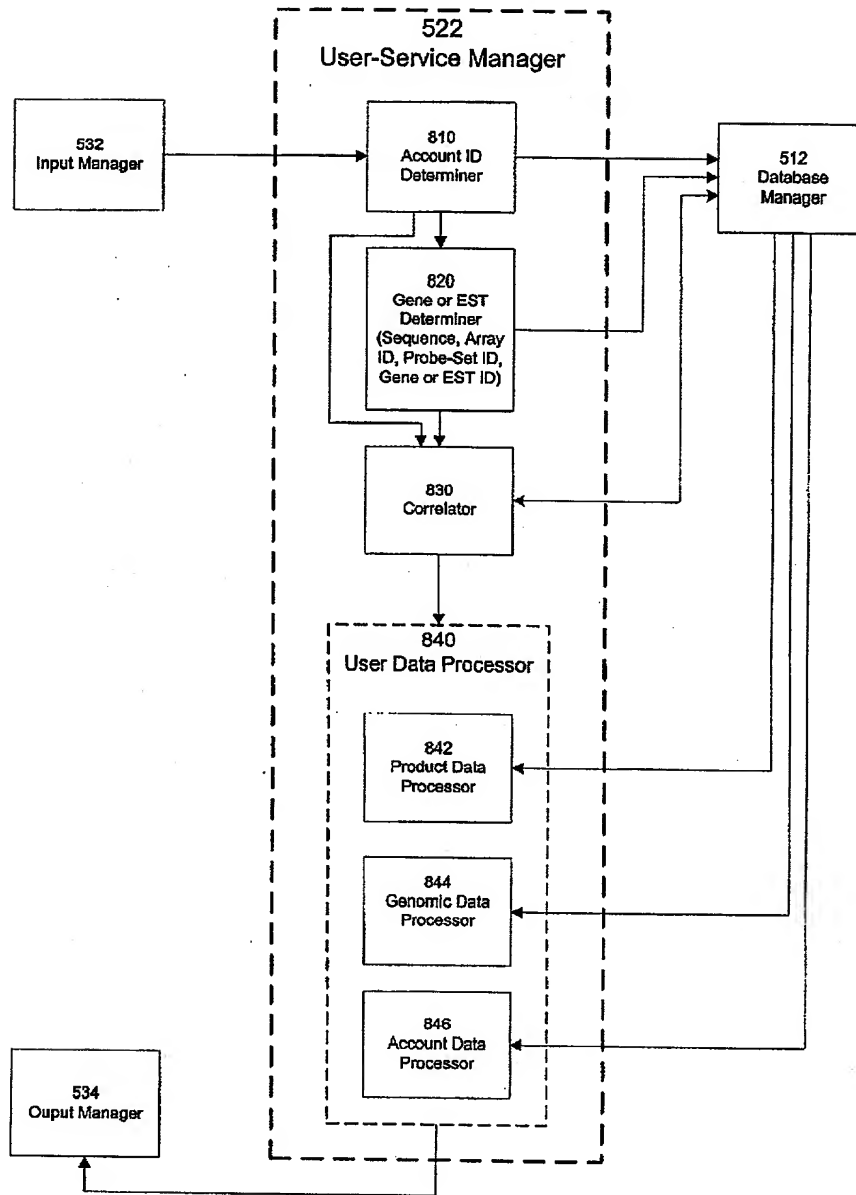


FIGURE 9

513
Gene or Probe-Set ID
to Products and/or
Genomics Databases

902 Gene or EST ID	904 Link to Probe-Set IDS 912
ID 902A	Link 904N
ID 902B	Link 904N
ID 902C	Link 904M

912 Probe-Set ID (accession #, sequence, etc.)	914 Array ID	916 Links to Related Product and/or Genomic Data IDs
Probe-Set 912A	Array 914N	Links 916A
Probe-Set 912B	Array 914N	Links 916B
Probe-Set 912C	Array 914P	Links 916C
Probe-Set 912D	Array 914Q	Links 916D
Probe-Set 912E	Array 914N	Links 916E

922 Product and/or Genomic Data ID	924 Link to Local Products Database 514 and/ or Genomic Database 518	926 Links to Vendor or Genomic Database Web Pages
Product/Genomic ID 922A	Link 924A	Links 926A
Product/Genomic ID 922B	Link 924B	Links 926B
Product/Genomic ID 922C	Link 924C	Links 926C
Product/Genomic ID 922C	Link 924D	Links 926D
Product/Genomic ID 922D	Link 924E	Links 926E

Figure 10

518
Local Genomic
and/or Product
Database

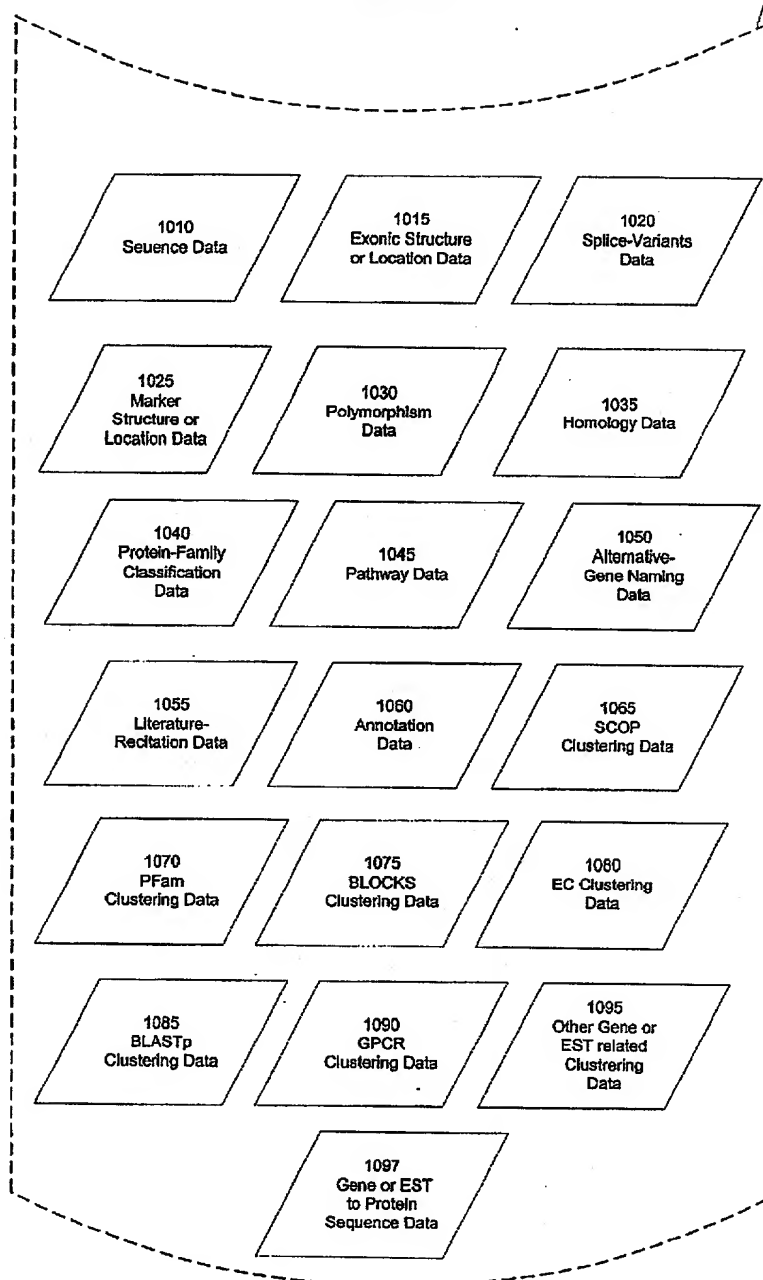


Figure 11

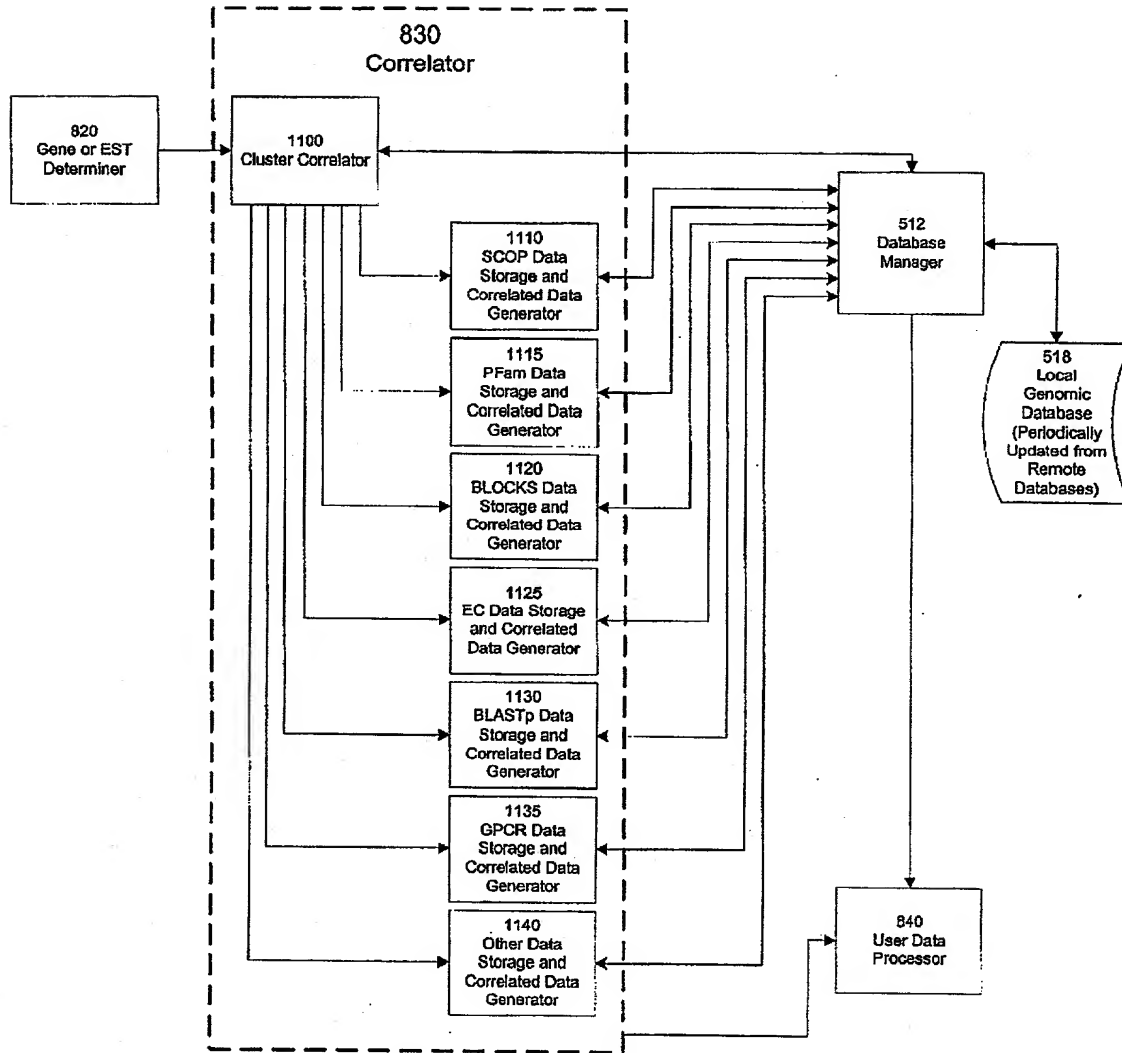


Figure 12

1200
GUI

1240
Protein Identifier

1210
Cluster Method Identifier

1220
Returned Family Data

1230
Returned Alignment Data

Domains PFAM Hs:NP_003828

ID NP_003828

SEARCH_METHOD hmmpfam

HIT_NAME FBpase WUSTL

HIT_DESC Fructose-1-6-bisphosphatase

OVERALL_EXPECT 1.5e-179 LOG10 -179

SIMSPAN Query 12 _ 335 Target 1 _ 342; EXPECT 1.5e-179 LOG10 -179;

ALIGNMENT

FBpase: domain 1 of 1, from 12 to 335: score 609.9, E = 1.5e-179

*->iTLtrfileeggedalAKNEatgeltddlLssLalaakeiartIarag

+TLtr ++e+ g+ a+ tgelt+lL+s +a k+i+++++ag

NP_003828 12 LTLTRYVMEK-GROAK----GTGELTQLLSMLTAIKAISSAVRKAG

53

LanllGlagatNsQGDeQKkLDViaddifinALKasgvvavlaSEEdel

La+l+G+ag++N++GDe+KkLDV+++ ++in+L++s ++vl+SEE+++

NP_003828 54 LAHLYGIAGSVNVTGDEVKLDVLSNSLVINMLQSSYSTCVLVSEENKDA

103

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